

SEQUENCE LISTING


<110> DECKERS, HARM M.
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BOOTHE, JOSEPH
GOLL, JANIS
MOLONEY, MAURICE M.
DALMIA, BIPIN K.

<160> THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
BODY BASED PRODUCTS

<130> 034547/0104

<140> 09/897,898
<141> 2001-07-05

<150> 09/577,147
<151> 2000-05-24

<150> 09/448,600
<151> 1999-11-24

<150> 09/084,777
<151> 1998-05-27

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<151> 1997-05-28

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<151> 1998-02-25

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<170> PatentIn Ver. 2.1

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thioredoxin reductase

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ggc cca gca cac acg gcg att tac gca gct agg gct gaa ctt 96
Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
20 25 30

aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt 144
Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
35 40 45

ggt caa cta aca acc acc gac gtc gag aat ttc ccc gga ttt cca 192
Gly Gln Leu Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
50 55 60

gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg 240
Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
65 70 75 80

gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat 288
Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
85 90 95

ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc 336
Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
100 105 110

gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc 384
Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
115 120 125

ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc 432
Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
130 135 140

tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa 480
Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145 150 155 160

cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gca aac 528
Pro Leu Ala Val Ile Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
165 170 175

ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat 576
Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
180 185 190

gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct 624
Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
195 200 205

aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat 672
Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
210 215 220

gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc		720
Gly Glu Arg Asp Val Leu Gly Leu Lys Val Lys Asn Val Val Thr		
225 230 235 240		
gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt		768
Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly		
245 250 255		
cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg		816
His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser		
260 265 270		
gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc		864
Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro		
275 280 285		
gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc		912
Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala		
290 295 300		
atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat		960
Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His		
305 310 315 320		
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Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp		
325 330		

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<220>
<221> CDS
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1 5 10 15		
ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt		96
Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu		
20 25 30		
aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt		144
Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly		
35 40 45		
ggt caa cta aca acc acc gac gtc gag aat ttc ccc gga ttt cca		192
Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro		
50 55 60		
gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg		240
Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser		
65 70 75 80		

gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat		288	
Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp			
85	90	95	
tcc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc		336	
Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu			
100	105	110	
gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc		384	
Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser			
115	120	125	
tcc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc		432	
Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile			
130	135	140	
tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa		480	
Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys			
145	150	155	160
cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac		528	
Pro Leu Ala Val Ile Gly Gly Asp Ser Ala Met Glu Glu Ala Asn			
165	170	175	
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Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp			
180	185	190	
gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct		624	
Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro			
195	200	205	
aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat		672	
Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp			
210	215	220	
gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc		720	
Gly Glu Arg Asp Val Leu Gly Leu Lys Val Lys Asn Val Val Thr			
225	230	235	240
gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt		768	
Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly			
245	250	255	
cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg		816	
His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser			
260	265	270	
gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc		864	
Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro			
275	280	285	
gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc		912	
Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala			
290	295	300	

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 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
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 20 25 30

Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
 35 40 45

Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
 50 55 60

Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
 65 70 75 80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
 85 90 95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110

Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125

Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
 145 150 155 160

Pro Leu Ala Val Ile Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
 165 170 175

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190

Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205

Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220

Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
 225 230 235 240

Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
 245 250 255

His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
 260 265 270

Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285

Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
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Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
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Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
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<212> PRT

<213> Unknown Organism

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<223> Description of Unknown Organism: Published NADPH
 thioredoxin reductase

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Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
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Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
 20 25 30

Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
 35 40 45

Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
 50 55 60

Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
 65 70 75 80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
 85 90 95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110

Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125

Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
 145 150 155 160

Pro Leu Ala Val Ile Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
 165 170 175

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190

Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205

Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220

Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
 225 230 235 240

Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
 245 250 255

His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
 260 265 270

Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285

Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
 290 295 300

Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
 305 310 315 320

Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

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 ttacttgta cttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaattt ttatgaagtc 240
 ccgtctatct ttaatgttagt ctaacatccc catattgaaa tatataatcc acttaatccc 300

agcgttggta gaaaggataa tgatttattc ttattcttct tcataataat gtttaatata 360
caatataaac aaattcttta ccttaagaag gatttcccat tttatattt aaaaatatat 420
ttatcaaata ttttcaacc acgtaaatct cataataata agttgttca aaagtaataa 480
aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
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aaatttcacc aaacaatcat ttgtggatt tctgaagcaa gtcatgttat gcaaaattct 660
ataattccca tttgacacta cggaagtaac tgaagatctg ctTTTACATG cgagacacat 720
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aattgttgaa ttgtgacta ttgatttatt attctactat gttaaattg ttttatacat 900
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cccacatctcaa cccacacaca aacacattgc ctTTTCTTC atcatcacca caaccacctg 1320
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actactctac tactataata ccccaaccca actcatattc aatactactc tact atg 1557
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1
gct tcg gaa gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg 1605
Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp
5 10 15
aac gag cag ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt 1653
Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val
20 25 30
gat ttc acg gct tct tgg tgg gga cca tgt cgt ttc atc gct cca ttc 1701
Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe
35 40 45

ttt gct gat ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt	1749
Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val	
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Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala	
70 75 80	
 atg cca acc ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt	1845
Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val	
85 90 95	
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Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu	
100 105 110	
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Ala	
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aacaattata aagagagaag tttgtatcca tttatataatt atatactacc catttatata	2366
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<213> Arabidopsis thaliana

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Val Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro
35 40 45

Phe Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys
50 55 60

Val Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln
65 70 75 80

Ala Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys
85 90 95

Val Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His
100 105 110

Leu Ala

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<213> Unknown Organism

<220>
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<222> (1555) .. (1908)

<220>
<221> CDS
<222> (2149) .. (2655)

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promoter-oleosin Trxh-phaseolin terminator

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tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

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 caatataaaac aaattCTTta ccttaagaag gatttcccattttt aaaaatataat 420
 ttatcaaata ttttcaacc acgtaaatct cataataata agttgttca aaagtaataa 480
 aatttaactc cataatTTT ttattcgact gatcttaaag caacacccag tgacacaact 540
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 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660
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 aattgttcaa ttgttgacta ttgatttattt attctactat gtttaaattt gtttatagat 900
 agtttaaagt aaatataagt aatgttagtag agtgttagag tgTTACCTTA aaccataaac 960
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 actactCTAC tactATAATA ccccaacCCA actCATATTc aataCTACTC tact ATG 1557
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 1

 gCG gat aca gct aga gga acc cat cac gat atc atc ggc aga gac cag 1605
 Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln
 5 10 15

 tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc gga cga 1653
 Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg
 20 25 30

 gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act gct 1701
 Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala
 35 40 45

gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt		1749	
Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val			
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gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc		1797	
Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe			
70	75	80	
agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc		1845	
Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr			
85	90	95	
ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc		1893	
Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe			
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tct tgg att tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa		1948	
Ser Trp Ile Tyr Lys			
115			
tatgtgcatg catgtgttga gccagtagct ttggatcaat tttttggc gaataacaaa		2008	
tgtaacaata agaaatttgc aattcttaggg aacatttggtaactaaata cgaaatttga		2068	
cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggatgtat		2128	
acctatttgc tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac		2181	
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp			
120	125		
aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg		2229	
Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu			
130	135	140	145
aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat		2277	
Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His			
150	155	160	
gac cgt gac cgt act cgt ggt ggc cag cac act acc atg gct tcg gaa		2325	
Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Ala Ser Glu			
165	170	175	
gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg aac gag cag		2373	
Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp Asn Glu Gln			
180	185	190	
ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt gat ttc acg		2421	
Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val Asp Phe Thr			
195	200	205	
gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc ttt gct gat		2469	
Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe Phe Ala Asp			
210	215	220	225
ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt gat act gat		2517	
Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val Asp Thr Asp			
230	235	240	

gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg atg cca acc	2565
Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala Met Pro Thr	
245	250
	255
ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt gtt gga gcc	2613
Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val Val Gly Ala	
260	265
	270
aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg gct	2655
Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu Ala	
275	280
	285
taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg agagcatgga	2715
atattgtatc cgaccatgta acagtataat aactgagctc catctcaactt cttctatgaa	2775
taaacaaagg atgttatgat atattaacac tctatctatg caccttattt ttctatgata	2835
aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gcttcaaata	2895
gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa	2955
cgagacataa gtgttaagaa gacataacaa ttataatgga agaagttgt ctccatttat	3015
atattatata ttacccactt atgtattata ttaggatgtt aaggagacat aacaattata	3075
aagagagaag tttgtatcca tttatataatt atatactacc catttatata ttatacttat	3135
ccacttattt aatgtcttta taaggtttga tccatgatat ttctaatatt ttagttgata	3195
tgtatatgaa agggtactat ttgaactctc ttactctgta taaaggttg atcatcctta	3255
aagtgggtct atttaatttt attgcttctt acagataaaaa aaaaaattat gagttggttt	3315
gataaaatata tgaaggattt aaaataataa taaataataa ataacatata atatatgtat	3375
ataaaatttat tataatataa catttatcta taaaaaaatgta aatattgtca taaatctata	3435
caatcgttta gccttgctgg acgactctca attatttaaa cgagagtaaa catatttgac	3495
tttttggtta tttaacaaat tattattaa cactatatga aattttttt ttttatcgcc	3555
aaggaaataa aattaaattha ggagggacaa tggtgtgtcc caatccttat acaaccaact	3615
tccacaggaa ggtcagggtcg gggacaacaa aaaaacaggc aaggaaatt tttaatttg	3675
ggttgtctt tttgctgcat aatttatgca gtaaaacact acacataacc ctttttagcag	3735
tagagcaatg gttgaccgtg tgcttagctt cttttatattt attttttat cagcaaagaa	3795
taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa accccaaaaaa	3855
caagttcct agcacccctac caactaaggt acc	3888

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
promoter-oleosin Trxh-phaseolin terminator

<400> 8

Met	Ala	Asp	Thr	Ala	Arg	Gly	Thr	His	His	Asp	Ile	Ile	Gly	Arg	Asp
1				5				10					15		

Gln	Tyr	Pro	Met	Met	Gly	Arg	Asp	Arg	Asp	Gln	Tyr	Gln	Met	Ser	Gly
				20				25				30			

Arg	Gly	Ser	Asp	Tyr	Ser	Lys	Ser	Arg	Gln	Ile	Ala	Lys	Ala	Ala	Thr
				35			40					45			

Ala	Val	Thr	Ala	Gly	Gly	Ser	Leu	Leu	Val	Leu	Ser	Ser	Leu	Thr	Leu
				50			55					60			

Val	Gly	Thr	Val	Ile	Ala	Leu	Thr	Val	Ala	Thr	Pro	Leu	Leu	Val	Ile
65				70				75				80			

Phe	Ser	Pro	Ile	Leu	Val	Pro	Ala	Leu	Ile	Thr	Val	Ala	Leu	Leu	Ile
				85				90				95			

Thr	Gly	Phe	Leu	Ser	Ser	Gly	Gly	Phe	Gly	Ile	Ala	Ala	Ile	Thr	Val
				100			105					110			

Phe	Ser	Trp	Ile	Tyr	Lys										
				115											

<210> 9

<211> 169

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
promoter-oleosin Trxh-phaseolin terminator

<400> 9

Tyr	Ala	Thr	Gly	Glu	His	Pro	Gln	Gly	Ser	Asp	Lys	Leu	Asp	Ser	Ala
1				5				10					15		

Arg	Met	Lys	Leu	Gly	Ser	Lys	Ala	Gln	Asp	Leu	Lys	Asp	Arg	Ala	Gln
				20				25				30			

Tyr	Tyr	Gly	Gln	Gln	His	Thr	Gly	Gly	Glu	His	Asp	Arg	Asp	Arg	Thr
35					40				45						

Arg	Gly	Gly	Gln	His	Thr	Thr	Met	Ala	Ser	Glu	Glu	Gly	Gln	Val	Ile
50					55							60			

Ala	Cys	His	Thr	Val	Glu	Thr	Trp	Asn	Glu	Gln	Leu	Gln	Lys	Ala	Asn
65					70				75				80		

Glu Ser Lys Thr Leu Val Val Asp Phe Thr Ala Ser Trp Cys Gly
 85 90 95

 Pro Cys Arg Phe Ile Ala Pro Phe Phe Ala Asp Leu Ala Lys Lys Leu
 100 105 110

 Pro Asn Val Leu Phe Leu Lys Val Asp Thr Asp Glu Leu Lys Ser Val
 115 120 125

 Ala Ser Asp Trp Ala Ile Gln Ala Met Pro Thr Phe Met Phe Leu Lys
 130 135 140

 Glu Gly Lys Ile Leu Asp Lys Val Val Gly Ala Lys Lys Asp Glu Leu
 145 150 155 160

 Gln Ser Thr Ile Ala Lys His Leu Ala
 165

<210> 10
 <211> 3888
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (1555)..(2250)

<220>
 <221> CDS
 <222> (2491)..(2655)

<220>
 <223> Description of Unknown Organism: Phaseolin
 promoter-Trxh oleosin-phaseolin terminator

<400> 10
 ctgcaggaat tcattgtact cccagtatca ttatagtcaa agttttggct ctctcgccgg 60

 tggttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120

 ttacttggta cttaatttc tcataatctt tggttgaat tatcacgctt ccgcacacga 180

 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300

 agcgttggta gaaagcataa tgatttattc ttattcttct tcataataat gtttaatata 360

 caatataaaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420

 ttatcaaata ttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480

 aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540

 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatTTTT tatacaatga 600

aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaaattct 660
 ataattccca tttgacacta cggaagttaac tgaagatctg cttttacatg cgagacacat 720
 cttctaaagt aattttata atagttacta tattcaagat ttcatatatc aaatactcaa 780
 tattacttct aaaaaattaa ttagatataa ttaaaatatt actttttaa ttttaagttt 840
 aattgtgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
 agtttaaagt aaatataagt aatgttagtag agtgttagag tgtaacccta aaccataaac 960
 tataagattt atggtggact aattttcata tatttcttat tgctttacc ttttcttgg 1020
 atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt ctttgggtc 1080
 atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
 acaaaaacgca atcacacaac caactcaa at tagtcaactgg ctgatcaaga tcgcccgcgc 1200
 catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260
 cccatctcaa cccacacaca aacacattgc cttttcttc atcatcacca caaccacctg 1320
 tatatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
 atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
 atacctataa atacctctaa tatcaactcac ttcttcatc atccatccat ccagagtact 1500
)
 actactctac tactataata ccccaaccca actcatatcc aataactactc tact atg 1557
 Met
 1
 gct tcg gaa gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg 1605
 Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp
 5 10 15
 aac gag cag ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt 1653
 Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val
 20 25 30
 gat ttc acg gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc 1701
 Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe
 35 40 45
 ttt gct gat ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt 1749
 Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val
 50 55 60 65
 gat act gat gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg 1797
 Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala
 70 75 80
 atg cca acc ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt 1845
 Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val
 85 90 95

gtt gga gcc aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu	1893
100 105 110	
 gct atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga Ala Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg	1941
115 120 125	
 gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser	1989
130 135 140 145	
 gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct gca Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala	2037
150 155 160	
 act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr	2085
165 170 175	
 ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val	2133
180 185 190	
 atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu	2181
195 200 205	
 atc acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc Ile Thr Gly Phe Leu Ser Ser Gly Phe Gly Ile Ala Ala Ile Thr	2229
210 215 220 225	
 gtt ttc tct tgg att tac aag taagcacaca tttatcatct tacttcataa Val Phe Ser Trp Ile Tyr Lys	2280
230	
 ttttgtgcaa tatgtgcattt catgtgttga gccagtagct ttggatcaat tttttggc gaataacaaa tgtaacaata agaaatttgc aattctagg aacatttggt taactaaata	2340
 cgaaaatttgc cctagcttagc ttgaatgtgt ctgtgttatcatctata ggtaaaaatgc	2400
 ttggtatgtatcatctata tttatcatctata tac gca acg gga gag cac cca cag Tyr Ala Thr Gly Glu His Pro Gln	2460
235 240	
 gga tca gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct Gly Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala	2514
245 250 255	
 cag gat ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly	2562
260 265 270	
 ggg gaa cat gac cgt gac cgt act cgt ggt ggc cag cac act act Gly Glu His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr	2610
275 280 285	

taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg agagcatgga 2715
 atattgtatc cgaccatgta acagtataat aactgagctc catctcaactt cttctatgaa 2775
 taaacaaagg atgttatgat atattaacac tctatctatg caccttattt ttctatgata 2835
 aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gcttcaaata 2895
 gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa 2955
 cgagacataa gtgttaagaa gacataacaa ttataatgga agaagttgt ctccatttat 3015
 atattatata ttacccactt atgtattata ttaggatgtt aaggagacat aacaattata 3075
 aagagagaag tttgtatcca tttatataat atatactacc catttatata ttatacttat 3135
 ccacttattt aatgtctta taaggttga tccatgatat ttctaataatt ttagttgata 3195
 tgtatatgaa agggtactat ttgaactctc ttactctgt aaaaaggtgg atcatcotta 3255
 aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat gagttggttt 3315
 gataaaatat tgaaggattt aaaataataa taaataataa ataacatata atatatgtat 3375
 ataaatttat tataatataa catttatcta taaaaaagta aatattgtca taaatctata 3435
 caatcggtta gccttgctgg acgactctca attatttaaa cgagagtaaa catattgac 3495
 tttttggta tttaacaaat tattatttaa cactatatga aattttttt ttttatcggc 3555
 aaggaaataa aattaaatta ggagggacaa tggtgtgtcc caatccttat acaaccaact 3615
 tccacaggaa ggtcaggtcg gggacaacaa aaaaacaggc aaggaaattt ttttaatttg 3675
 ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc ctttttagcag 3735
 tagagcaatg gttgaccgtg tgcttagctt cttttatttt attttttat cagcaaagaa 3795
 taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa accccaaaaaa 3855
 caagtttcct agcaccctac caactaaggt acc 3888

<210> 11
 <211> 232
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Phaseolin
 promoter-Trxh oleosin-phaseolin terminator

<400> 11
 Met Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr
 1 5 10 15

Trp Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val
 20 25 30

Val	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ala	Pro
35									40						45
Phe	Phe	Ala	Asp	Leu	Ala	Lys	Lys	Leu	Pro	Asn	Val	Leu	Phe	Leu	Lys
50								55						60	
Val	Asp	Thr	Asp	Glu	Leu	Lys	Ser	Val	Ala	Ser	Asp	Trp	Ala	Ile	Gln
65								70						75	
Ala	Met	Pro	Thr	Phe	Met	Phe	Leu	Lys	Glu	Gly	Lys	Ile	Leu	Asp	Lys
85										90					95
Val	Val	Gly	Ala	Lys	Lys	Asp	Glu	Leu	Gln	Ser	Thr	Ile	Ala	Lys	His
100										105					110
Leu	Ala	Met	Ala	Asp	Thr	Ala	Arg	Gly	Thr	His	His	Asp	Ile	Ile	Gly
115								120						125	
Arg	Asp	Gln	Tyr	Pro	Met	Met	Gly	Arg	Asp	Arg	Asp	Gln	Tyr	Gln	Met
130								135						140	
Ser	Gly	Arg	Gly	Ser	Asp	Tyr	Ser	Lys	Ser	Arg	Gln	Ile	Ala	Lys	Ala
145								150						155	
Ala	Thr	Ala	Val	Thr	Ala	Gly	Gly	Ser	Leu	Leu	Val	Leu	Ser	Ser	Leu
165										170					175
Thr	Leu	Val	Gly	Thr	Val	Ile	Ala	Leu	Thr	Val	Ala	Thr	Pro	Leu	Leu
180									185						190
Val	Ile	Phe	Ser	Pro	Ile	Leu	Val	Pro	Ala	Leu	Ile	Thr	Val	Ala	Leu
195									200						205
Leu	Ile	Thr	Gly	Phe	Leu	Ser	Ser	Gly	Gly	Phe	Gly	Ile	Ala	Ala	Ile
210									215						220
Thr	Val	Phe	Ser	Trp	Ile	Tyr	Lys								
225									230						

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr
50 55

<210> 13
<211> 3787
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1555) .. (2553)

<220>
<223> Description of Unknown Organism: Phaseolin
promoter-thioredoxin reductase-phaseolin
terminator

<400> 13
ctgcaggaat tcattgtact cccagtatca ttatagtcaa agttttggct ctctcgccgg 60
tggttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120
ttacttgta ctttaatttc tcataatctt tggttgaat tatcacgctt ccgcacacga 180
tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaattt ttatgaagtc 240
ccgtctatct ttaatgttgt ctaacatccc catattgaaa tatataatcc acttaatccc 300
agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatata 360
caatataaac aaattcttta ccttaagaag gatcccattttt aaaaatata 420
ttatcaaata ttttcaacc acgtaaatct cataataata agttttca aaagtaataa 480
aatttaactc cataatcccc ttattcgact gatcttaaag caacacccag tgacacaact 540
agccatcccc ttctttgaat aaaaaatcc aattatcatt gtatcccc tatacatga 600
aaatttcacc aaacaatcat ttgtggatt tctgaagcaa gtcatgttat gcaaaattct 660
ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
cttctaaagt aattttata atagttacta tattcaagat ttcatatatac aaataactcaa 780
tattacttct aaaaaattaa tttagatataa taaaatattt actttttaa ttttaagttt 840
aattgttgaa ttgttgacta ttgattttt attctactat gtttaaattt gtttataagat 900
agtttaaagt aaatataagt aatgttagtag agtgttagag tgttacccta aaccataaac 960
tataagattt atgggtggact aattttcata tatttcttat tgctttacc ttttcttggt 1020
atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttgggttc 1080

atgcatggat gcttcgcaaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
acaaaacgca atcacacaac caactcaa at tagtcactgg ctgatcaaga tcgcccgtc 1200
catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260
cccatctcaa cccacacaca aacacattgc cttttcttc atcatcacca caaccacctg 1320
tatatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacacctcat 1380
atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
atacctataa atacctctaa tatcactcac ttcttcatc atccatccat ccagagtact 1500
actactctac tactataata ccccaaccca actcatattc aatactactc tact atg 1557
Met
1
aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt ggc 1605
Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly
5 10 15
cca gcg gca cac acg gcg att tac gca gct agg gct gaa ctt aaa 1653
Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys
20 25 30
cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt 1701
Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly
35 40 45
caa cta aca acc acc gac gtc gag aat ttc ccc gga ttt cca gaa 1749
Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu
50 55 60 65
ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag 1797
Gly Ile Leu Gly Val Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu
70 75 80
cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc 1845
Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe
85 90 95
tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct 1893
Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala
100 105 110
gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc ttc 1941
Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe
115 120 125
gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc 1989
Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser
130 135 140 145
gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct 2037
Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro
150 155 160

ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt	2085
Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe	
165 170 175	
ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat gct	2133
Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala	
180 185 190	
ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct aag	2181
Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys	
195 200 205	
att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga	2229
Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly	
210 215 220 225	
gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga	2277
Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly	
230 235 240	
gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat	2325
Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His	
245 250 255	
gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat	2373
Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp	
260 265 270	
ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc gga	2421
Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly	
275 280 285	
gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc	2469
Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile	
290 295 300 305	
act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat tac	2517
Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr	
310 315 320	
tta caa gag att gga tct cag caa ggt aag agt gat tgaagcttaa	2563
Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp	
325 330	
taagtatgaa ctaaatgca tgttagtgta agagctcatg gagagcatgg aatattgtat	2623
ccgaccatgt aacagtataa taactgagct ccatctcaact tcttctatga ataaacaaaag	2683
gatgttatga tatattaaca ctctatctat gcaccttatt gttctatgat aaatttcctc	2743
tttattattt aaatcatctg aatcgtgacg gcttatggaa tgcttcaaatt agtacaaaaaa	2803
caaatgtgta ctataagact ttctaaacaa ttctaaacttt agcattgtga acgagacata	2863
agtgttaaga agacataaca attataatgg aagaagttt tctccattta tatatttat	2923
attacccact tatgttattt attaggatgt taaggagaca taacaattat aaagagagaa	2983

gtttgttatcc atttatata tataactac ccatttat attatactta tccacttatt 3043
taatgtctt ataaggttt atccatgata tttctaata ttttagttgat atgtatatga 3103
aagggtacta ttgaaactct cttactctgt ataaagggtt gatcatcctt aaagtgggtc 3163
tatthaattt tattgcttct tacagataaa aaaaaaatta tgagttggtt tgataaaaata 3223
ttgaaggatt taaaataata ataaataata aataacatata aatataatgta tataaattta 3283
ttataatata acatttatct ataaaaaaagt aaatattgtc ataaatctat acaatcggtt 3343
agccttgctg gacgactctc aattattna acgagagtaa acatatttga cttttgggtt 3403
atthaacaaa ttattattna acactatata aatttttt ttttatcgg caaggaaata 3463
aaattaaattt aggagggaca atggtgtgtc ccaatcctt tacaaccaac ttccacagga 3523
aggtcagggtc ggggacaaca aaaaaacagg caagggaaat ttttaattt gggttgtctt 3583
gtttgctgca taatttatgc agtaaaacac tacacataac ccttttagca gtagagcaat 3643
ggttgaccgt gtgcttagct tcttttattt tatttttttca tcagcaaaga ataaataaaa 3703
taaaaatgaga cacttcaggg atgttcaac ccttatacaa aaccccaaaa acaagttcc 3763
tagcacccca ccaactaagg tacc 3787

<210> 14
<211> 333
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Phaseolin promoter-thioredoxin reductase-phaseolin terminator

<400> 14
Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
1 5 10 15

Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
20 25 30

Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
 35 40 45

Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
50 55 60

Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
65 70 75 80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
85 90 95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110
 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125
 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140
 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
 145 150 155 160
 Pro Leu Ala Val Ile Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
 165 170 175
 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190
 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205
 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220
 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
 225 230 235 240
 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
 245 250 255
 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
 260 265 270
 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285
 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
 290 295 300
 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
 305 310 315 320
 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

<210> 15
 <211> 4546
 <212> DNA
 <213> Unknown Organism

 <220>
 <221> CDS
 <222> (1555)..(1908)

<220>
<221> CDS
<222> (2149) .. (3312)

<220>
<223> Description of Unknown Organism: Phaseolin
promoter-oleosin thioredoxin reductase-phaseolin
terminator

<400> 15
ctgcaggaat tcattgtact cccagtatca ttatagtcaa agttttggct ctctgcgg 60
tggttttta cctctattta aagggtttt ccacctaaaa attctggtat cattctca 120
ttacttgtta cttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
agcgttgta gaaagcataa tgatttattc ttattcttct tcatataat gtttaatata 360
caatataaac aaattcttta ccttaagaag gatttccat tttatattt aaaaatat 420
ttatcaaata ttttcaacc acgtaaatct cataataata agttttca aaagtaataa 480
aatttaactc cataattttt ttattcgact gatcttaag caacacccag tgacacaact 540
agccattttt ttctttgaat aaaaaatcc aattatcatt gtatTTTT tatacatga 600
aaatttcacc aaacaatcat ttgtggatt tctgaagcaa gtcatgttat gcaaaattct 660
ataattccca tttgacacta cggaagtaac tgaagatctg ctttacatg cgagacacat 720
cttctaaagt aattttata atagttacta tattcaagat ttcatatatc aaatactcaa 780
tattacttct aaaaaattaa ttagatataa taaaatatt actttttaa tttaagttt 840
aattgttgaa ttgttgacta ttgatttatt attctactat gttaaattg tttttagat 900
agtttaaagt aaatataagt aatgttagtag agtggtagag tgttacccta aaccataaac 960
tataagattt atggtgact aattttcata tatttcttac tgctttacc ttttcttgg 1020
atgttaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt ctgggg 1080
atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
acaaaacgca atcacacaac caactcaaata tagtcactgg ctgatcaaga tcggcg 1200
catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcactt aaatggctca 1260
cccacatctcaa cccacacaca aacacattgc cttttcttc atcatcacca caaccacctg 1320
tatatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccccttct ctcttatata 1440

gac cgt gac cgt act cgt ggt ggc cag cac act acc atg aat ggt ctc		2325	
Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Asn Gly Leu			
165	170	175	
gaa act cac aac aca agg ctc tgt atc gta gga agt ggc cca gcg gca		2373	
Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly Pro Ala Ala			
180	185	190	
cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa cct ctt ctc		2421	
His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys Pro Leu Leu			
195	200	205	
ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt caa cta aca		2469	
Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly Gln Leu Thr			
210	215	220	225
acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa ggt att ctc		2517	
Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu Gly Ile Leu			
230	235	240	
gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag cga ttc ggt		2565	
Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu Arg Phe Gly			
245	250	255	
act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc tct tcg aaa		2613	
Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe Ser Ser Lys			
260	265	270	
ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct gac gct gtg		2661	
Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala Asp Ala Val			
275	280	285	
att ctc gct act gga gct gtg gct aag cgg ctt agc ttc gtt gga tct		2709	
Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe Val Gly Ser			
290	295	300	305
ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc gct tgt gct		2757	
Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala			
310	315	320	
gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct ctt gcg gtg		2805	
Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro Leu Ala Val			
325	330	335	
atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt ctt aca aaa		2853	
Ile Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys			
340	345	350	
tat gga tct aaa gtg tat ata atc cat agg aga gat gct ttt aga gcg		2901	
Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala Phe Arg Ala			
355	360	365	
tct aag att atg cag cag cga gct ttg tct aat cct aag att gat gtg		2949	
Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys Ile Asp Val			
370	375	380	385

att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga gaa aga gat Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly Glu Arg Asp 390 395 400	2997
gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga gat gtt tct Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly Asp Val Ser 405 410 415	3045
gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat gag cca gct Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala 420 425 430	3093
acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat ggt tat gtt Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp Gly Tyr Val 435 440 445	3141
gtc acg aag cct ggt act aca cag act agc gtt ccc gga gtt ttc gct Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly Val Phe Ala 450 455 460 465	3189
gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc act gct gca Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala 470 475 480	3237
gga act ggg tgc atg gca gct ttg gat gca gag cat tac tta caa gag Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu 485 490 495	3285
att gga tct cag caa ggt aag agt gat tgaaggctaa taagtatgaa Ile Gly Ser Gln Gln Gly Lys Ser Asp 500 505	3332
<p>ctaaaatgca ttaggtgta agagctcatg gagagcatgg aatattgtat ccgaccatgt 3392</p> <p>aacagtataa taactgagct ccatctcact tcttcttatga ataaacaaag gatgttatga 3452</p> <p>tatattaaca ctctatctat gcaccttatt gttctatgat aaatttcctc ttattattat 3512</p> <p>aaatcatctg aatcggtacg gcttatggaa tgcttcaaattt agtacaaaaaa caaatgtgta 3572</p> <p>ctataagact ttctaaacaa ttcttaacttt agcattgtga acgagacata agtgttaaga 3632</p> <p>agacataaca attataatgg aagaagttt tctccattta tatattatattt attacccact 3692</p> <p>tatgtattat attaggatgt taaggagaca taacaattat aaagagagaa gtttgatcc 3752</p> <p>atttatatat tatatactac ccatttatattt attatactta tccacttattt taatgtctt 3812</p> <p>ataaggtttt atccatgata ttcttaatattt tttagttgat atgtatatga aagggtacta 3872</p> <p>tttgaactct cttactctgt ataaagggttg gatcatcctt aaagtgggtc tatttaattt 3932</p> <p>tattgcttct tacagataaaa aaaaaattt tgagttgggtt tgataaaaata ttgaaggatt 3992</p> <p>taaaataata ataaataata aataacatattt aatataatgta tataaattta ttataatata 4052</p> <p>acatttatct ataaaaaaagt aaatattgtc ataaatctat acaatcgttt agccttgctg 4112</p>	

gacgactctc aattatcaa acgagagtaa acatatggta cttttgggtt atttaacaaa 4172
 ttattatcta acactatatg aaattttttt ttttatcggtt caaggaaata aaattaaattt 4232
 aggagggaca atggtgtgtc ccaatccctta tacaaccaac ttccacagga aggtcaggc 4292
 ggggacaaca aaaaaacagg caagggaaat ttttaattt gggttgtctt gtttgctgca 4352
 taatttatgc agtaaaacac tacacataac ccttttagca gtagagcaat gggtgaccgt 4412
 gtgcttagct tcttttattt tatttttta tcagcaaaga ataaataaaa taaaatgaga 4472
 cacttcaggg atgttcaac ccttatacaa aaccccaaaa acaagttcc tagcacccta 4532
 ccaactaagg tacc 4546

<210> 16
 <211> 118
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Phaseolin
 promoter-oleosin thioredoxin reductase-phaseolin
 terminator

<400> 16
 Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
 1 5 10 15
 Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
 20 25 30
 Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
 35 40 45
 Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
 50 55 60
 Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
 65 70 75 80
 Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
 85 90 95
 Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
 100 105 110
 Phe Ser Trp Ile Tyr Lys
 115

<210> 17
 <211> 388
 <212> PRT
 <213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
promoter-oleosin thioredoxin reductase-phaseolin
terminator

<400> 17

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45Arg Gly Gly Gln His Thr Thr Met Asn Gly Leu Glu Thr His Asn Thr
50 55 60Arg Leu Cys Ile Val Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile
65 70 75 80Tyr Ala Ala Arg Ala Glu Leu Lys Pro Leu Leu Phe Glu Gly Trp Met
85 90 95Ala Asn Asp Ile Ala Pro Gly Gly Gln Leu Thr Thr Thr Asp Val
100 105 110Glu Asn Phe Pro Gly Phe Pro Glu Gly Ile Leu Gly Val Glu Leu Thr
115 120 125Asp Lys Phe Arg Lys Gln Ser Glu Arg Phe Gly Thr Thr Ile Phe Thr
130 135 140Glu Thr Val Thr Lys Val Asp Phe Ser Ser Lys Pro Phe Lys Leu Phe
145 150 155 160Thr Asp Ser Lys Ala Ile Leu Ala Asp Ala Val Ile Leu Ala Thr Gly
165 170 175Ala Val Ala Lys Arg Leu Ser Phe Val Gly Ser Gly Glu Gly Ser Gly
180 185 190Gly Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala
195 200 205Ala Pro Ile Phe Arg Asn Lys Pro Leu Ala Val Ile Gly Gly Asp
210 215 220Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Lys Val
225 230 235 240Tyr Ile Ile His Arg Arg Asp Ala Phe Arg Ala Ser Lys Ile Met Gln
245 250 255Gln Arg Ala Leu Ser Asn Pro Lys Ile Asp Val Ile Trp Asn Ser Ser
260 265 270

Val Val Glu Ala Tyr Gly Asp Gly Glu Arg Asp Val Leu Gly Gly Leu
 275 280 285
 Lys Val Lys Asn Val Val Thr Gly Asp Val Ser Asp Leu Lys Val Ser
 290 295 300
 Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Asp
 305 310 315 320
 Gly Gly Val Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro Gly
 325 330 335
 Thr Thr Gln Thr Ser Val Pro Gly Val Phe Ala Ala Gly Asp Val Gln
 340 345 350
 Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Thr Gly Cys Met
 355 360 365
 Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Ile Gly Ser Gln Gln
 370 375 380
 Gly Lys Ser Asp
 385

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<210> 18
<211> 4545
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1555) .. (2907)

<220>
<221> CDS
<222> (3148) .. (3312)

<220>
<223> Description of Unknown Organism: Phaseolin
      promoter-thioredoxin reductase oleosin-phaseolin
      terminator

<400> 18
ctgcaggaat tcattgtact cccagtatca ttatagtcaa agttttggct ctctcgccgg 60
tggttttta cctctattna aagggtttt ccacctaaaa attctggtat cattctcact 120
ttacttgta cttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
ccgtctatct ttaatgttgt ctaacattt catattgaaa tatataattt acttaattt 300
agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gttaatata 360
caatataaac aaattcttta ccttaagaag gattccccat tttatattt aaaaatatat 420
  
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ttatcaaata ttttcaacc acgtaaatct cataataata agttgttca aaagtaataa 480
 aatttaactc cataattttt ttattcgact gatcttaag caacacccag tgacacaact 540
 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatTTTT tatacatga 600
 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660
 ataattccca tttgacacta cggaagtaac tgaagatctg ctttacatg cgagacacat 720
 cttctaaagt aattttata atagttacta tattcaagat ttcatatatc aaatactcaa 780
 tattacttct aaaaaattaa ttagatataa taaaatatt actttttaa ttttaagttt 840
 aattgtgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttataagat 900
 agtttaaagt aaatataagt aatgttagtag agtgttagag tgtaacccta aaccataaac 960
 tataagattt atggtgact aattttcata tatttcttat tgctttacc ttttcttgg 1020
 atgtaagtcc gtaactggaa ttactgtggg tgcctatggc actctgtggt ctttgggtc 1080
 atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
 acaaaacgca atcacacaac caactcaa at tagtcactgg ctgatcaaga tcgcccgcgtc 1200
 catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260
 cccatctcaa cccacacaca aacacattgc cttttcttc atcatcacca caaccacctg 1320
 tatatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
 atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
 atacctataa atacctctaa tatcactcac ttcttcatc atccatccat ccagagtact 1500
 actactctac tactataata ccccaaccca actcatattc aatactactc tact atg 1557
 Met
 1
 aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt ggc 1605
 Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly
 5 10 15
 cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa 1653
 Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys
 20 25 30
 cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt 1701
 Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly
 35 40 45
 caa cta aca acc acc gac gtc gag aat ttc ccc gga ttt cca gaa 1749
 Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu
 50 55 60 65

ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag		1797	
Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu			
70	75	80	
cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc		1845	
Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe			
85	90	95	
tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct		1893	
Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala			
100	105	110	
gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc ttc		1941	
Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe			
115	120	125	
gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc		1989	
Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser			
130	135	140	145
gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct		2037	
Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro			
150	155	160	
ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt		2085	
Leu Ala Val Ile Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe			
165	170	175	
ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat gct		2133	
Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala			
180	185	190	
ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct aag		2181	
Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys			
195	200	205	
att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga		2229	
Ile Asp Val Ile Trp Asn Ser Val Val Glu Ala Tyr Gly Asp Gly			
210	215	220	225
gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga		2277	
Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly			
230	235	240	
gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat		2325	
Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His			
245	250	255	
gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat		2373	
Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp			
260	265	270	
ggg tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc gga		2421	
Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly			
275	280	285	

gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile 290 295 300 305	2469
act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat tac Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr 310 315 320	2517
tta caa gag att gga tct cag caa ggt aag agt gat atg gcg gat aca Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp Met Ala Asp Thr 325 330 335	2565
gct aga gga acc cat cac gat atc atc ggc aga gac cag tac ccg atg Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met 340 345 350	2613
atg ggc cga gac cga gac cag tac cag atg tcc gga cga gga tct gac Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp 355 360 365	2661
tac tcc aag tct agg cag att gct aaa gct gca act gct gtc aca gct Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala 370 375 380 385	2709
ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt gga act gtc Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val 390 395 400	2757
ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc agc cca atc Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile 405 410 415	2805
ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc ggt ttt ctt Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu 420 425 430	2853
tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc tct tgg att Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile 435 440 445	2901
tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa tatgtgcattg Tyr Lys 450	2957
catgtgttga gccagtagct ttggatcaat tttttggtc gaataacaaa tgtaacaata agaaatttgc aattctaggg aacatttggt taactaaata cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtttatgc ttggatgtat acctattgtat tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac aag ttg Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu 455 460	3137
gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg aaa gac Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp 465 470 475 480	3186
gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg aaa gac Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp 465 470 475 480	3234

aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat gac cgt 3282
Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg
485 490 495

gac cgt act cgt ggt ggc cag cac act act taagcttaat aagtatgaac 3332
Asp Arg Thr Arg Gly Gly Gln His Thr Thr
500 505

taaaaatgcat gtaggtgtaa gagctcatgg agagcatgga atattgtatc cgaccatgta 3392
acagtataat aactgagctc catctcaactt cttcttatgaa taaacaaagg atgttatgat 3452
atattaacac tctatctatg caccttatttg ttcttatgata aatttcctct tattattata 3512
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aatttatgca gtaaaaacact acacataacc ctttttagcag tagagcaatg gttgaccgtg 4412
tgcttagctt cttttatattt attttttat cagcaaagaa taaataaaaat aaaatgagac 4472
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caactaaggtt acc 4545

<210> 19
<211> 451
<212> PRT
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
promoter-thioredoxin reductase oleosin-phaseolin
terminator

<400> 19

Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
1 5 10 15Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
20 25 30Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
35 40 45Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
50 55 60Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
65 70 75 80Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
85 90 95Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
100 105 110Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
115 120 125Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
130 135 140Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145 150 155 160Pro Leu Ala Val Ile Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
165 170 175Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
180 185 190Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
195 200 205Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
210 215 220Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225 230 235 240Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
245 250 255His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
260 265 270

Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285

Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
 290 295 300

Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
 305 310 315 320

Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp Met Ala Asp
 325 330 335

Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln Tyr Pro
 340 345 350

Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser
 355 360 365

Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala Val Thr
 370 375 380

Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly Thr
 385 390 395 400

Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser Pro
 405 410 415

Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly Phe
 420 425 430

Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe Ser Trp
 435 440 445

Ile Tyr Lys
 450

<210> 20
 <211> 55
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Phaseolin
 promoter-thioredoxin reductase oleosin-phaseolin
 terminator

<400> 20
 Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
 1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
 20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
 35 40 45

Arg Gly Gly Gln His Thr Thr
50 55

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
taccatggct tcggaagaag ga

22

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
gaaagcttaa gccaaagtgtt tg

22

<210> 23
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
ggccagcaca ctaccatgaa tggtctcgaa actcac

36

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
ttaagcttca atcactctta ctttgctg

28